

## SEQUENCE LISTING

&lt;110&gt; Johnson et al.

<120> INHIBITION OF THE MHC CLASS II ANTIGEN PRESENTATION  
PATHWAY AND PRESENTATION TO CD4+ CELLS

&lt;130&gt; 0899-54203 Johnson

&lt;140&gt;

&lt;141&gt;

&lt;150&gt; 60/118,287

&lt;151&gt; 1999-02-02

&lt;160&gt; 7

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 600

&lt;212&gt; DNA

&lt;213&gt; Cytomegalovirus

&lt;400&gt; 1

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tcagcacacg aaaaaccgca tccacatcat agacaagtta cagtccacag tcacatacac 60
gataaacaat accaacaggg taatgtttat ggagtaaaac actattgtcc aggccacatg 120
cgtgtatgac ttccgcacca tcccgtactg catgttccac atgtacgcgc tagacgtgta 180
atccactcgc agttcgggga cgcaacgcag ccagatcaca tccccttgca gtaccagacg 240
cagggctagc gtctcgaaga tcggcatcac atctaagttc cgcacgttcc actttaacga 300
ctccccggga acgaactcca cgtcgtcggc gtgtacgtac aggttctctc ccacgccgcc 360
ataatcgcc ttccgatcga agacgaaccg actcatgttg cccacgatgc tcccccgagc 420
aaacaacttg ccgttgtcaa tgtagcaccg gttgtcctcg atttgaaacc agggatgctt 480
ggcgcgtggac ttccagggcc ggagcgcgctc ttccccggct ttagtgattc catcgggcag 540
gcggatcaag ggacccatgg aggtccaaag acccaccag gctttccaga gattgttcat 600

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&lt;210&gt; 2

&lt;211&gt; 600

&lt;212&gt; DNA

&lt;213&gt; Cytomegalovirus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(600)

&lt;400&gt; 2

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atg aac aat ctc tgg aaa gcc tgg gtg ggt ctt tgg acc tcc atg ggt 48
Met Asn Asn Leu Trp Lys Ala Trp Val Gly Leu Trp Thr Ser Met Gly
  1             5             10             15

ccc ttg atc cgc ctg ccc gat gga atc act aaa gcc ggg gaa gac gcg 96
Pro Leu Ile Arg Leu Pro Asp Gly Ile Thr Lys Ala Gly Glu Asp Ala
      20             25             30

ctc cgg ccc tgg aag tcc acg gcc aag cat ccc tgg ttt caa atc gag 144
Leu Arg Pro Trp Lys Ser Thr Ala Lys His Pro Trp Phe Gln Ile Glu
      35             40             45

gac aac cgg tgc tac att gac aac ggc aag ttg ttt gct cgg ggg agc 192

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Asp Asn Arg Cys Tyr Ile Asp Asn Gly Lys Leu Phe Ala Arg Gly Ser  
 50 55 60  
 atc gtg ggc aac atg agt cgg ttc gtc ttc gat ccg aag gcc gat tat 240  
 Ile Val Gly Asn Met Ser Arg Phe Val Phe Asp Pro Lys Ala Asp Tyr  
 65 70 75 80  
 ggc ggc gtg gga gag aac ctg tac gta cac gcc gac gac gtg gag ttc 288  
 Gly Gly Val Gly Glu Asn Leu Tyr Val His Ala Asp Asp Val Glu Phe  
 85 90 95  
 gtt ccc ggg gag tcg tta aag tgg aac gtg cgg aac tta gat gtg atg 336  
 Val Pro Gly Glu Ser Leu Lys Trp Asn Val Arg Asn Leu Asp Val Met  
 100 105 110  
 ccg atc ttc gag acg cta gcc ctg cgt ctg gta ctg caa ggg gat gtg 384  
 Pro Ile Phe Glu Thr Leu Ala Leu Arg Leu Val Leu Gln Gly Asp Val  
 115 120 125  
 atc tgg ctg cgt tgc gtc ccc gaa ctg cga gtg gat tac acg tct agc 432  
 Ile Trp Leu Arg Cys Val Pro Glu Leu Arg Val Asp Tyr Thr Ser Ser  
 130 135 140  
 gcg tac atg tgg aac atg cag tac ggg atg gtg cgg aag tca tac acg 480  
 Ala Tyr Met Trp Asn Met Gln Tyr Gly Met Val Arg Lys Ser Tyr Thr  
 145 150 155 160  
 cat gtg gcc tgg aca ata gtg ttt tac tcc ata aac att acc ctg ttg 528  
 His Val Ala Trp Thr Ile Val Phe Tyr Ser Ile Asn Ile Thr Leu Leu  
 165 170 175  
 gta ttg ttt atc gtg tat gtg act gtg gac tgt aac ttg tct atg atg 576  
 Val Leu Phe Ile Val Tyr Val Thr Val Asp Cys Asn Leu Ser Met Met  
 180 185 190  
 tgg atg cgg ttt ttc gtg tgc tga 600  
 Trp Met Arg Phe Phe Val Cys  
 195 200

&lt;210&gt; 3

&lt;211&gt; 199

&lt;212&gt; PRT

&lt;213&gt; Cytomegalovirus

&lt;400&gt; 3

Met Asn Asn Leu Trp Lys Ala Trp Val Gly Leu Trp Thr Ser Met Gly  
 1 5 10 15  
 Pro Leu Ile Arg Leu Pro Asp Gly Ile Thr Lys Ala Gly Glu Asp Ala  
 20 25 30  
 Leu Arg Pro Trp Lys Ser Thr Ala Lys His Pro Trp Phe Gln Ile Glu  
 35 40 45  
 Asp Asn Arg Cys Tyr Ile Asp Asn Gly Lys Leu Phe Ala Arg Gly Ser  
 50 55 60  
 Ile Val Gly Asn Met Ser Arg Phe Val Phe Asp Pro Lys Ala Asp Tyr  
 65 70 75 80  
 Gly Gly Val Gly Glu Asn Leu Tyr Val His Ala Asp Asp Val Glu Phe  
 85 90 95  
 Val Pro Gly Glu Ser Leu Lys Trp Asn Val Arg Asn Leu Asp Val Met  
 100 105 110

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Pro Ile Phe•Glu Thr Leu Ala Leu Arg Leu Val Leu Gln Gly Asp Val
      115      120      125
Ile Trp Leu Arg Cys Val Pro Glu Leu Arg Val Asp Tyr Thr Ser Ser
      130      135      140
Ala Tyr Met Trp Asn Met Gln Tyr Gly Met Val Arg Lys Ser Tyr Thr
145      150      155      160
His Val Ala Trp Thr Ile Val Phe Tyr Ser Ile Asn Ile Thr Leu Leu
      165      170      175
Val Leu Phe Ile Val Tyr Val Thr Val Asp Cys Asn Leu Ser Met Met
      180      185      190
Trp Met Arg Phe Phe Val Cys
      195

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&lt;210&gt; 4

&lt;211&gt; 534

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: chimera

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(534)

&lt;400&gt; 4

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atg aaa ttc tta gtc aac gtt gcc ctt gtt ttt atg gtc gtg tac att 48
Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
  1          5          10          15

tct tac atc tat gcg cgc ctg ccc gat gga atc act aaa gcc ggg gaa 96
Ser Tyr Ile Tyr Ala Arg Leu Pro Asp Gly Ile Thr Lys Ala Gly Glu
          20          25          30

gac gcg ctc cgg ccc tgg aag tcc acg gcc aag cat ccc tgg ttt caa 144
Asp Ala Leu Arg Pro Trp Lys Ser Thr Ala Lys His Pro Trp Phe Gln
          35          40          45

atc gag gac aac cgg tgc tac att gac aac ggc aag ttg ttt gct cgg 192
Ile Glu Asp Asn Arg Cys Tyr Ile Asp Asn Gly Lys Leu Phe Ala Arg
          50          55          60

ggg agc atc gtg ggc aac atg agt cgg ttc gtc ttc gat ccg aag gcc 240
Gly Ser Ile Val Gly Asn Met Ser Arg Phe Val Phe Asp Pro Lys Ala
          65          70          75          80

gat tat ggc ggc gtg gga gag aac ctg tac gta cac gcc gac gac gtg 288
Asp Tyr Gly Gly Val Gly Glu Asn Leu Tyr Val His Ala Asp Asp Val
          85          90          95

gag ttc gtt ccc ggg gag tcg tta aag tgg aac gtg cgg aac tta gat 336
Glu Phe Val Pro Gly Glu Ser Leu Lys Trp Asn Val Arg Asn Leu Asp
          100          105          110

gtg atg ccg atc ttc gag acg cta gcc ctg cgt ctg gta ctg caa ggg 384
Val Met Pro Ile Phe Glu Thr Leu Ala Leu Arg Leu Val Leu Gln Gly
          115          120          125

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gat gtg atc tgg ctg cgt tgc gtc ccc gaa ctg cga gtg gat tac acg 432  
 Asp Val Ile Trp Leu Arg Cys Val Pro Glu Leu Arg Val Asp Tyr Thr  
 130 135 140

tct agc gcg tac atg tgg aac atg cag tac ggg atg gtg ggg cag cca 480  
 Ser Ser Ala Tyr Met Trp Asn Met Gln Tyr Gly Met Val Gly Gln Pro  
 145 150 155 160

gaa ctc gcc ccg gaa gac ccc gag gat tcg gcc ctc ttg gag gac ccc 528  
 Glu Leu Ala Pro Glu Asp Pro Glu Asp Ser Ala Leu Leu Glu Asp Pro  
 165 170 175

gtg tga 534  
 Val

<210> 5  
 <211> 177  
 <212> PRT  
 <213> Artificial Sequence  
 <223> Description of Artificial Sequence: chimera

<400> 5  
 Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile  
 1 5 10 15  
 Ser Tyr Ile Tyr Ala Arg Leu Pro Asp Gly Ile Thr Lys Ala Gly Glu  
 20 25 30  
 Asp Ala Leu Arg Pro Trp Lys Ser Thr Ala Lys His Pro Trp Phe Gln  
 35 40 45  
 Ile Glu Asp Asn Arg Cys Tyr Ile Asp Asn Gly Lys Leu Phe Ala Arg  
 50 55 60  
 Gly Ser Ile Val Gly Asn Met Ser Arg Phe Val Phe Asp Pro Lys Ala  
 65 70 75 80  
 Asp Tyr Gly Gly Val Gly Glu Asn Leu Tyr Val His Ala Asp Asp Val  
 85 90 95  
 Glu Phe Val Pro Gly Glu Ser Leu Lys Trp Asn Val Arg Asn Leu Asp  
 100 105 110  
 Val Met Pro Ile Phe Glu Thr Leu Ala Leu Arg Leu Val Leu Gln Gly  
 115 120 125  
 Asp Val Ile Trp Leu Arg Cys Val Pro Glu Leu Arg Val Asp Tyr Thr  
 130 135 140  
 Ser Ser Ala Tyr Met Trp Asn Met Gln Tyr Gly Met Val Gly Gln Pro  
 145 150 155 160  
 Glu Leu Ala Pro Glu Asp Pro Glu Asp Ser Ala Leu Leu Glu Asp Pro  
 165 170 175  
 Val

<210> 6  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Oligonucleotide

<400> 6  
 cgcgatcca tgaacaatct ctggaaagcc tgg 33

<210> 7

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide

<400> 7

cgtgaattcg acatgacaca cgtaatgggt act

33

09890806-114604  
T097T" 90806860

SEQUENCE LISTING

<110> Johnson et al.

<120> INHIBITION OF THE MHC CLASS II ANTIGEN PRESENTATION  
 PATHWAY AND PRESENTATION TO CD4+ CELLS

<130> 0899-59399

<140>

<141>

<150> US00/02740

<151> 2000-02-02

<150> 60/118,287

<151> 1999-02-02

<160> 7

<170> PatentIn Ver. 2.1

<210> 1

<211> 600

<212> DNA

<213> Cytomegalovirus

<400> 1

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gataaacaat accaacaggg taatgtttat ggagtaaaac actattgtcc aggccacatg 120
cgtgtatgac ttccgcacca tcccgtagtg catgttccac atgtacgcgc tagacgtgta 180
atccactcgc agttcgggga cgcaacgcag ccagatcaca tccccttgca gtaccagacg 240
cagggctagc gtctcgaaga tcggcatcac atctaagttc cgcacgttcc actttaacga 300
ctccccggga acgaactcca cgtcgtcggc gtgtacgtac aggttctctc ccacgccgcc 360
ataatcggcc ttccggatcga agacgaaccg actcatgttg cccacgatgc tcccccgagc 420
aaacaacttg ccgttgtcaa tgtagcacgc gttgtcctcg atttgaaacc agggatgctt 480
ggccgtggac ttccagggcc ggagcgcgtc ttccccgggt ttagtgattc catcgggcag 540
gcggatcaag ggacccatgg aggtccaaag acccaccagc gctttccaga gattgttcat 600
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<210> 2

<211> 600

<212> DNA

<213> cytomegalovirus

<220>

<221> CDS

<222> (1)..(600)

<400> 2

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atg aac aat ctc tgg aaa gcc tgg gtg ggt ctt tgg acc tcc atg ggt 48
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  1             5             10             15

ccc ttg atc cgc ctg ccc gat gga atc act aaa gcc ggg gaa gac gcg 96
Pro Leu Ile Arg Leu Pro Asp Gly Ile Thr Lys Ala Gly Glu Asp Ala
      20             25             30
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ctc cgg ccc tgg aag tcc acg gcc aag cat ccc tgg ttt caa atc gag	144
Leu Arg Pro Trp Lys Ser Thr Ala Lys His Pro Trp Phe Gln Ile Glu	
35 40 45	
gac aac cgg tgc tac att gac aac ggc aag ttg ttt gct cgg ggg agc	192
Asp Asn Arg Cys Tyr Ile Asp Asn Gly Lys Leu Phe Ala Arg Gly Ser	
50 55 60	
atc gtg ggc aac atg agt cgg ttc gtc ttc gat ccg aag gcc gat tat	240
Ile Val Gly Asn Met Ser Arg Phe Val Phe Asp Pro Lys Ala Asp Tyr	
65 70 75 80	
ggc ggc gtg gga gag aac ctg tac gta cac gcc gac gac gtg gag ttc	288
Gly Gly Val Gly Glu Asn Leu Tyr Val His Ala Asp Asp Val Glu Phe	
85 90 95	
gtt ccc ggg gag tcg tta aag tgg aac gtg cgg aac tta gat gtg atg	336
Val Pro Gly Glu Ser Leu Lys Trp Asn Val Arg Asn Leu Asp Val Met	
100 105 110	
ccg atc ttc gag acg cta gcc ctg cgt ctg gta ctg caa ggg gat gtg	384
Pro Ile Phe Glu Thr Leu Ala Leu Arg Leu Val Leu Gln Gly Asp Val	
115 120 125	
atc tgg ctg cgt tgc gtc ccc gaa ctg cga gtg gat tac acg tct agc	432
Ile Trp Leu Arg Cys Val Pro Glu Leu Arg Val Asp Tyr Thr Ser Ser	
130 135 140	
gcg tac atg tgg aac atg cag tac ggg atg gtg cgg aag tca tac acg	480
Ala Tyr Met Trp Asn Met Gln Tyr Gly Met Val Arg Lys Ser Tyr Thr	
145 150 155 160	
cat gtg gcc tgg aca ata gtg ttt tac tcc ata aac att acc ctg ttg	528
His Val Ala Trp Thr Ile Val Phe Tyr Ser Ile Asn Ile Thr Leu Leu	
165 170 175	
gta ttg ttt atc gtg tat gtg act gtg gac tgt aac ttg tct atg atg	576
Val Leu Phe Ile Val Tyr Val Thr Val Asp Cys Asn Leu Ser Met Met	
180 185 190	
tgg atg cgg ttt ttc gtg tgc tga	600
Trp Met Arg Phe Phe Val Cys	
195 199	

<210> 3  
 <211> 199  
 <212> PRT  
 <213> cytomegalovirus

<400> 3  
 Met Asn Asn Leu Trp Lys Ala Trp Val Gly Leu Trp Thr Ser Met Gly  
 1 5 10 15  
 Pro Leu Ile Arg Leu Pro Asp Gly Ile Thr Lys Ala Gly Glu Asp Ala  
 20 25 30  
 Leu Arg Pro Trp Lys Ser Thr Ala Lys His Pro Trp Phe Gln Ile Glu





gat tat ggc ggc gtg gga gag aac ctg tac gta cac gcc gac gac gtg	288
Asp Tyr Gly Gly Val Gly Glu Asn Leu Tyr Val His Ala Asp Asp Val	
85 90 95	
gag ttc gtt ccc ggg gag tcg tta aag tgg aac gtg cgg aac tta gat	336
Glu Phe Val Pro Gly Glu Ser Leu Lys Trp Asn Val Arg Asn Leu Asp	
100 105 110	
gtg atg ccg atc ttc gag acg cta gcc ctg cgt ctg gta ctg caa ggg	384
Val Met Pro Ile Phe Glu Thr Leu Ala Leu Arg Leu Val Leu Gln Gly	
115 120 125	
gat gtg atc tgg ctg cgt tgc gtc ccc gaa ctg cga gtg gat tac acg	432
Asp Val Ile Trp Leu Arg Cys Val Pro Glu Leu Arg Val Asp Tyr Thr	
130 135 140	
tct agc gcg tac atg tgg aac atg cag tac ggg atg gtg ggg cag cca	480
Ser Ser Ala Tyr Met Trp Asn Met Gln Tyr Gly Met Val Gly Gln Pro	
145 150 155 160	
gaa ctc gcc ccg gaa gac ccc gag gat tcg gcc ctc ttg gag gac ccc	528
Glu Leu Ala Pro Glu Asp Pro Glu Asp Ser Ala Leu Leu Glu Asp Pro	
165 170 175	
gtg tga	534
Val	

<210> 5  
 <211> 177  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:chimera

<400> 5
Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
1 5 10 15
Ser Tyr Ile Tyr Ala Arg Leu Pro Asp Gly Ile Thr Lys Ala Gly Glu
20 25 30
Asp Ala Leu Arg Pro Trp Lys Ser Thr Ala Lys His Pro Trp Phe Gln
35 40 45
Ile Glu Asp Asn Arg Cys Tyr Ile Asp Asn Gly Lys Leu Phe Ala Arg
50 55 60
Gly Ser Ile Val Gly Asn Met Ser Arg Phe Val Phe Asp Pro Lys Ala
65 70 75 80
Asp Tyr Gly Gly Val Gly Glu Asn Leu Tyr Val His Ala Asp Asp Val
85 90 95
Glu Phe Val Pro Gly Glu Ser Leu Lys Trp Asn Val Arg Asn Leu Asp
100 105 110
Val Met Pro Ile Phe Glu Thr Leu Ala Leu Arg Leu Val Leu Gln Gly
115 120 125
Asp Val Ile Trp Leu Arg Cys Val Pro Glu Leu Arg Val Asp Tyr Thr
130 135 140
Ser Ser Ala Tyr Met Trp Asn Met Gln Tyr Gly Met Val Gly Gln Pro
145 150 155 160

Glu Leu Ala Pro Glu Asp Pro Glu Asp Ser Ala Leu Leu Glu Asp Pro  
 165 170 175  
 Val

<210> 6  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:oligonucleotide

<400> 6  
 cgcggatcca tgaacaatct ctggaaagcc tgg 33

<210> 7  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:oligonucleotide

<400> 7  
 cgtgaattcg acatgacaca cgtaatgggt act 33